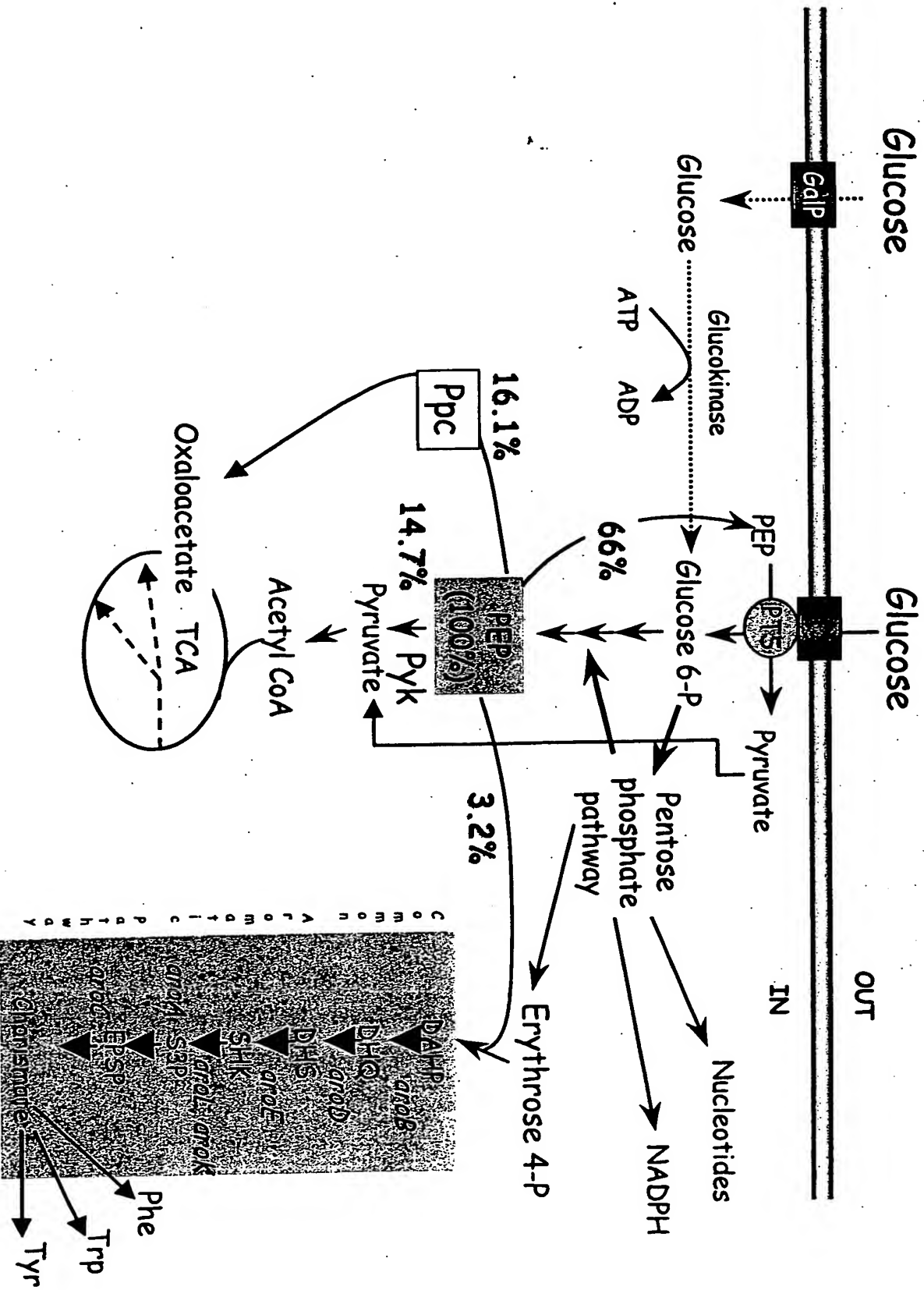


FIG. 1A



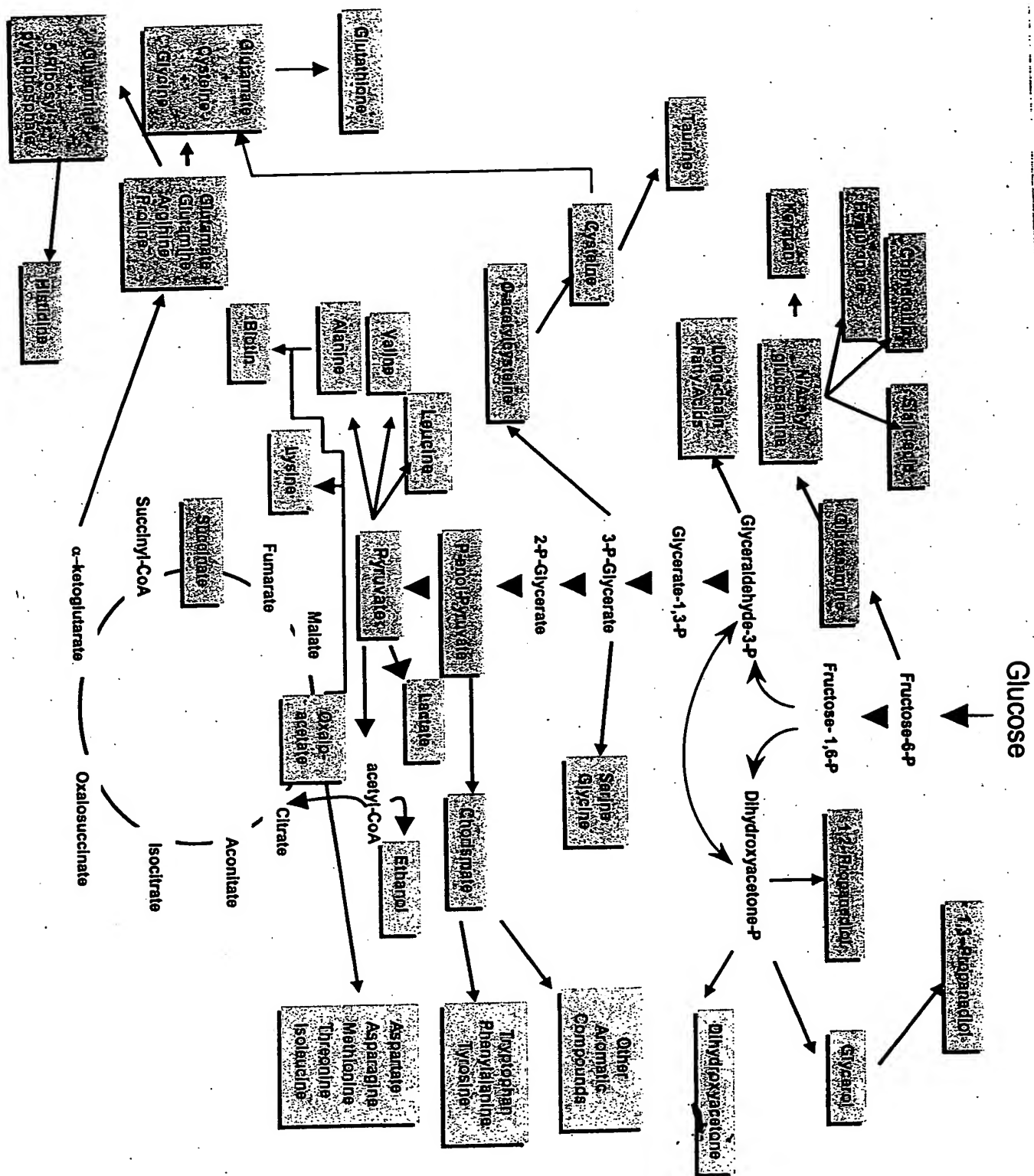


FIG. 2

TCGGTTTTACAGTTGTTACATTTCTTTTCAGTAAAGTCTGGATGCATATGGC
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AGCACCAGGCGTTTAAGGGCACCAATAACTGCCTTAAAAAAATTACGCCCC
GCCCTGCCACTCATCGCAGTACTGTTGTAATTCATTAAGCATTCTGCCGA
CATGGAAGCCATCACAAACGGCATGATGAACCTGAATCGCCAGCGGCAT
CAGCACCTTGTCGCCTTGCGTATAATATTTGCCCATGGTGAAAACGGGG
GCGAAGAAGTTGTCCATATTGGCCACGTTTAAATCAAACTGGTGAAAC
TCACCCAGGGATTGGCTGAGACGAAAAACATATTCTCAATAAACCCCTT
GGGAAATAGGCCAGGTTTTACCGTAACACGCCACATCTTGCGAATATA
TGTGTAGAACTGCCGGAAATCGTCGTGGTATTCACTCCAGAGCGATGA
AAACGTTTCAGTTTGCTCATGGAAAACGGTGTAACAAGGGTGAACTA
TCCCATATCACCAGCTCACCGTCTTTCATTGCCATACGGAATTCCGGATG
AGCATTTCATCAGGCGGGCAAGAATGTGAATAAAGGCCGGATAAACTTG
TGCTTATTTTTCTTTACGGTCTTTAAAAAGGCCGTAATATCCAGCTGAAC
GGTCTGGTTATAGGTACATTGAGCAACTGACTGAAATGCCTCAAAATGTT
CTTTACGATGCCATTGGGATATATCAACGGTGGTATATCCAGTGATTTTT
TTCTCCATTTTAGCTTCCTTAGCTCCTGAAAATCTCGATAACTCAAAAATAC
GCCCGGTAGTGATCTTATTTCAATTATGGTGAAAGTTGGAACCTCTTACGTGCC
GATCAACGTCTCATTTTCGCCAAAAGTTGGCCCAGGGCTTCCCGGTATCAACA
GGGACACCAGGATTTATTTATTCTGCGAAGTGATCTTCCGTCACAGGTATTTA
TTCGGACTCTAGATAACTTCGTATAGCATACATTATACGAAGTTATGGATCATG
GCTGTGCAGGTGCTAAATCACTGCATAATTCGTGTCGCTCAAGGCGCACTCCC
GTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTTCTGGCAAATATTCT
GAAATGAGCTGTTGACAATTAATCATCCGGCTCGTATAATGTGTGGAATTGTG
AGCGGATAACAATTTACACACAGGAAACAGACTAATTCACAATAAAAAATAACC
ATATTGGAGGGGCATCATG

FIG. 3

CAGCAGTGGTGGTGATCGGTTTTGGCTGGGGCCCCTCCCCGCACCGGAG
GCCGATTACAGCCAACCACAACAGGCAAAGGGTTTGGAAGATATTCATA
TTATTATTGCGGTTGTCACAGTTGTTACATTTCTTTTCAGTAAAGTCTGG
ATGCATATGGCGGCCCGCATAACTTCGTATAGCATAACATTATACGAAGTTATGGATC
ATGGCTGTGCAGGTCGTAAATCACTGCATAATTGGTGTGCTCAAGGCGCACT
CCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTTCTGGCAAATATT
CTGAAATGAGCTGTTGACAATTAATCATCCGGCTCGTATAATGTGTGGCATTG

FIG. 4

ACTTAGTTTGCCCAGCTTGCAAAAAGGCATCGCTGCAATTGGATGCATATGG
CGGCCGCATAACTTCGTATAGCATACATTATACGAAGTTATCTAGAGTTGCATG
CCTGCAGGTCCGAATTTCTGCCATTCATCCGCTTATTATCACTTATTCAGGCGT
AGCACCAGGCGTTTAAGGGCACCAATAACTGCCTTAAAAAAATTACGCCCC
GCCCTGCCACTCATCGCAGTACTGTTGTAATTCATTAAGCATTCTGCCGA
CATGGAAGCCATCACAACGGCATGATGAACCTGAATCGCCAGCGGCAT
CAGCACCTTGTCGCCTTGCGTATAATATTTGCCCATGGTGAAAACGGGG
GCGAAGAAGTTGTCCATATTGGCCACGTTTAAATCAAAACTGGTGAAAC
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GGTCTGGTTATAGGTACATTGAGCAACTGACTGAAATGCCTCAAAATGTT
CTTTACGATGCCATTGGGATATATCAACGGTGGTATATCCAGTGATTTTT
TTCTCCATTTTAGCTTCCTTAGCTCCTGAAAATCTCGATAACTCAAAAATAC
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GTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTTCTGGCAAATATTCT
GAAATGAGCTGCTGACAATTAATCATCCGGCTCGTATAATGTGTGGAATTGTG
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AGCGGAGCAGTTGAAGAATG

FIG. 5

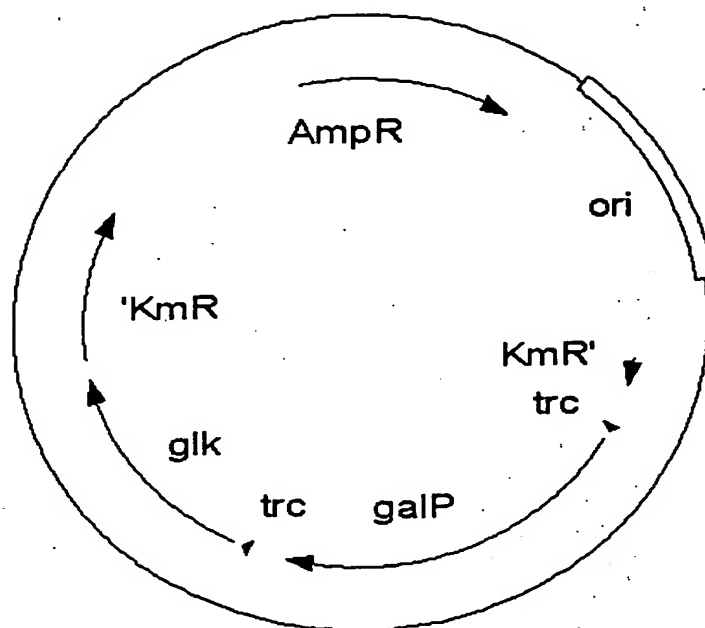


FIG. 6

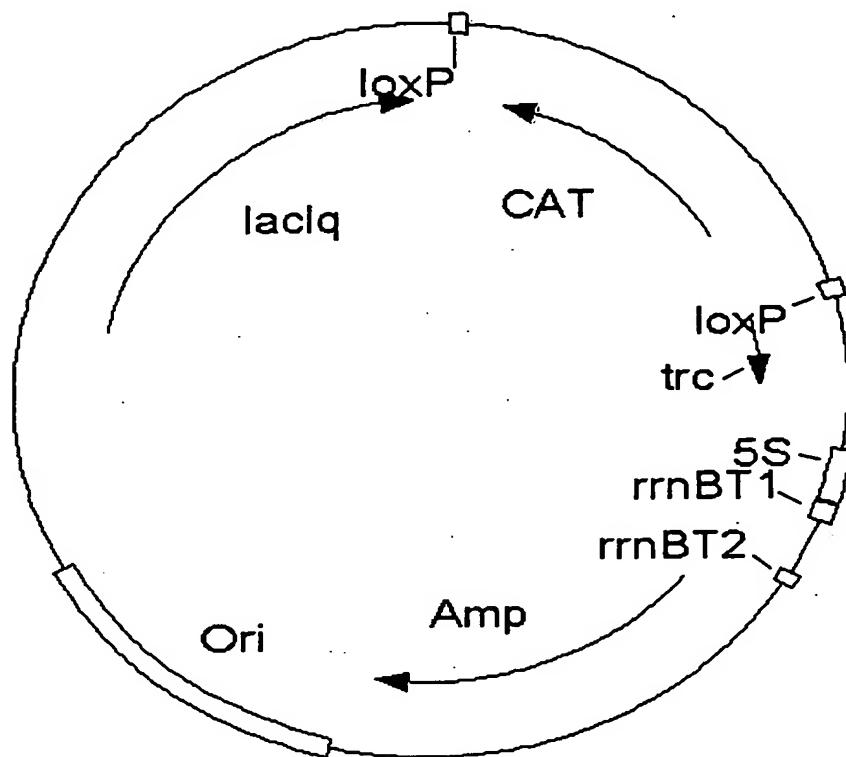


FIG. 7A.

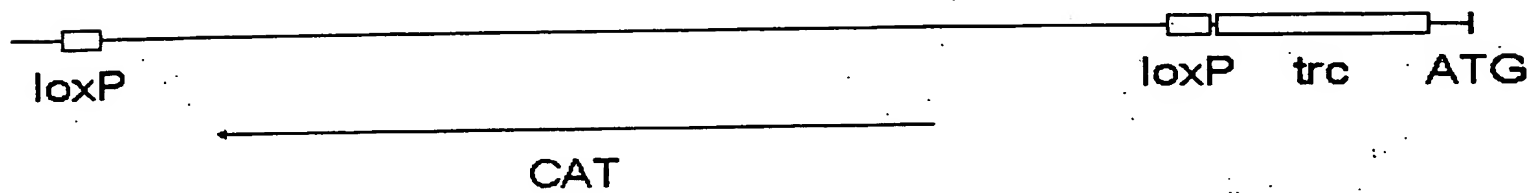


FIG. 7B

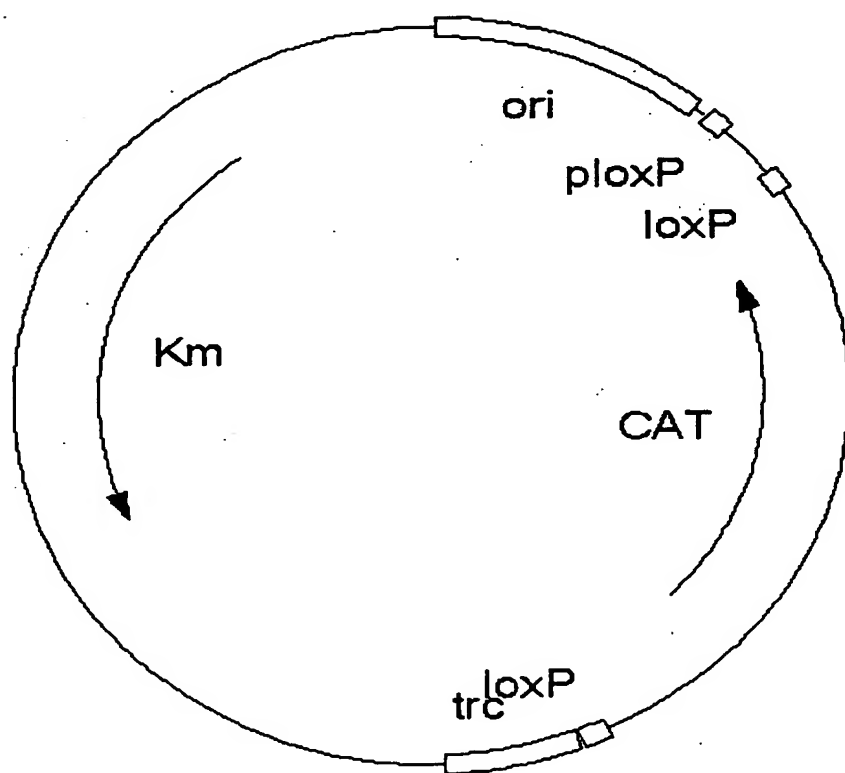


FIG. 8.

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GTCCAAGATAAGCCTGTCTAGCTTCAAGTATGACGGGCTGATACTGGGCCGGCAG
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TGTTTCTTCTCTAGATTCTGGGAAAAACATTTGACCGAATCTGATGATCTCACCCAA
ACCGACTCTTTGGATGGCAGCAGAAGCGTTGTTACCCAGCCTAGACCTTCGACGA
AACCACAACCTAAGGCAACAACGTTCTTCAAAGCACCACAGATGGAGATACCAGCA
ACATCTTCGATGACACTAACGTGGAAGTAAGGTCTGTGGAACAAGGCCTTTAGAAC
CTTATGGTCGACGTCCTTGCCCTCGCCTCTGAAATCCTTTGGAATGTGGTAAGCAA
CTGTTGTTTCAGACCAGTGTTCTTGAGCGACTTCGGTGGCAATGTTAGCACCAGAT
AGAGCACCACATTGAATACCTAGTTCCTCAGTGATGTAAGAGGATAGCAATTGGAC
ACCTTTAGCACCAACTTCAAAACCCTTTAGACAGGAGATAGCTCTGACGTGTGAATC
AACATGACCTTTCAATTGGCTACAGATACGGGGCAAAAATTGATGTGGAATGTTGAA
AACGATGATGTCGACATCCTTGACTGAATCAATCAAGTCTGGATTAGCAACCAAATT
GTCGGGTAGAGTGATGCCAGGCAAGTATTTACGTTTTGATGTCTAGTATTTATGAT
TTCAGTCAATTTTTACCATTTGATCTCTTCTTCGAACACCCACATTTGTACTATTGGA
GCGAAAACCTTCTGGGTATCCCTTACAATTTTCGGCAACCACCTTGGCAATAGTAGTA

CCCCAGTTACCAGATCCAATCACAGTAACCTTGAAAGGCTTTTCGGCAGCCTTCAA
AGAAACAGAAGAGGAACTTCTCTTTCTACCAGCATTCAAGTGGCCGGAAGTTAAGT
TTAATCTATCAGCAGCAGCAGCCATGGAATTGTCCTCCTTACTAGTCATGGTCTGTT
TCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACATTATACGAGCCGGATGATT
AATTGTCAACAGCTCATTTCAGAATATTTGCCAGAACC GTTATGATGTCGGCGCAAA
AAACATTATCCAGAACGGGAGTGCGCCTTGAGCGACACGAATTATGCAGTGATTTA
CGACCTGCACAGCCATACCACAGCTTCCGATGGCTGCCTGACGCCAGAAGCATTG
GTGCACGCTAGCCAGTACATTTAAATGGTACCCTCTAGTCAAGGCCTTAAGTGAGT
CGTATTACGGACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTT
ACCCA ACTTAATCGCCTTG CAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGA
AGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGG
CGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTACACCCGCATATG
GTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACC
CGCCAACACCCGCTGACGAGCT

FIG. 9

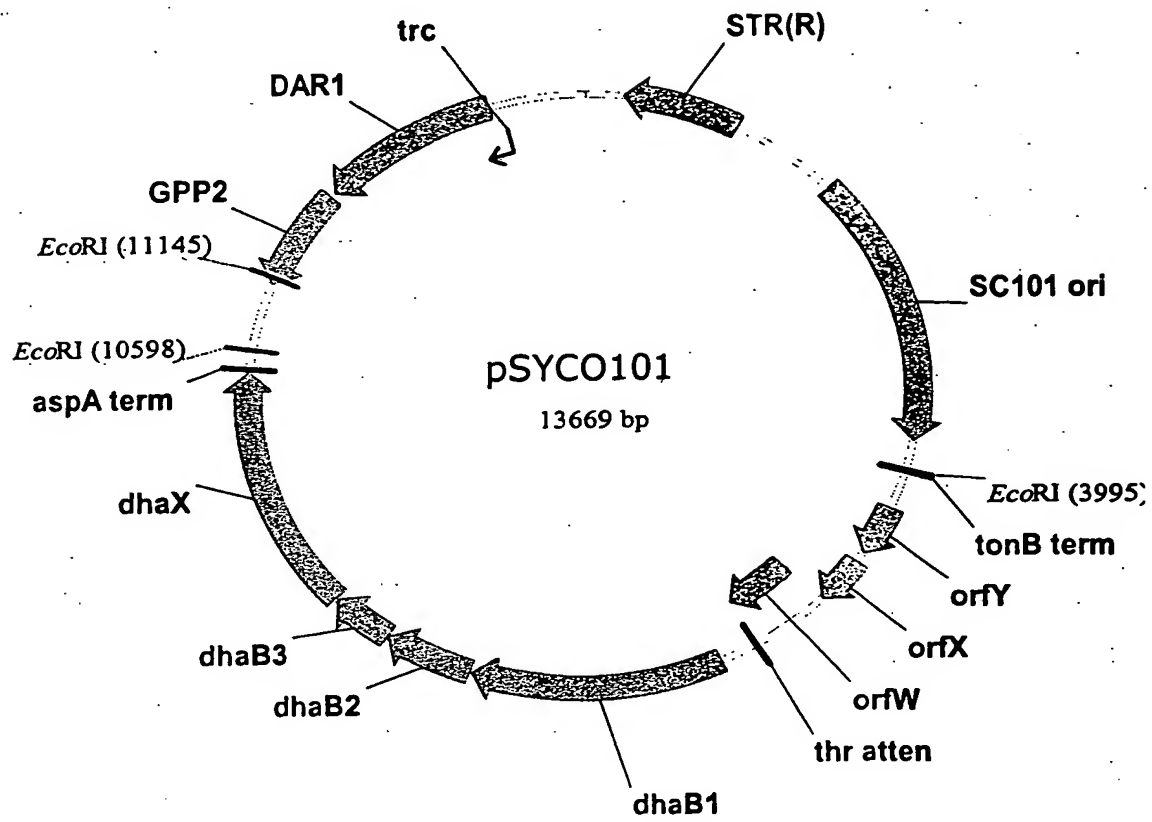
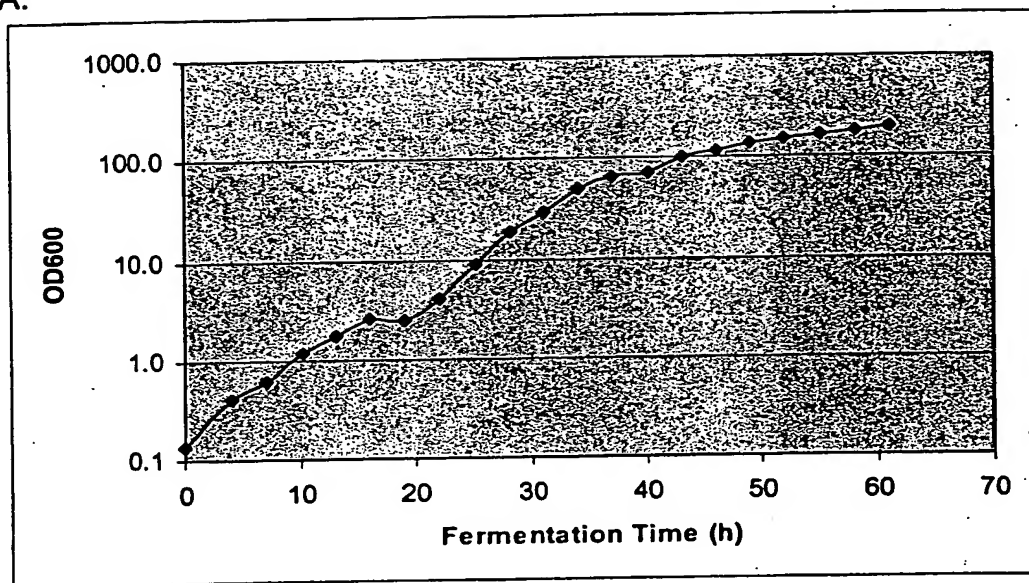


FIG. 10.

A.



B.

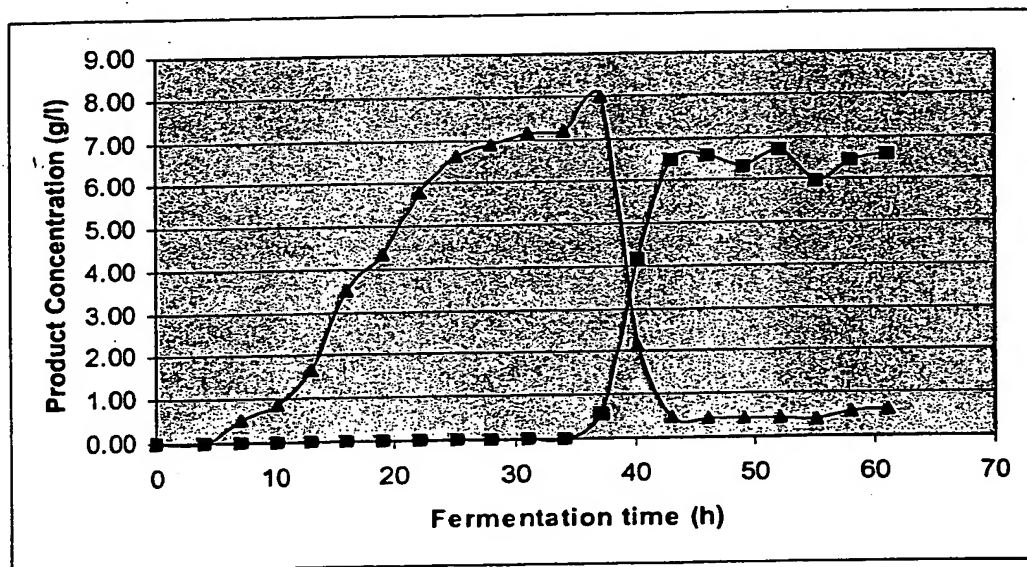
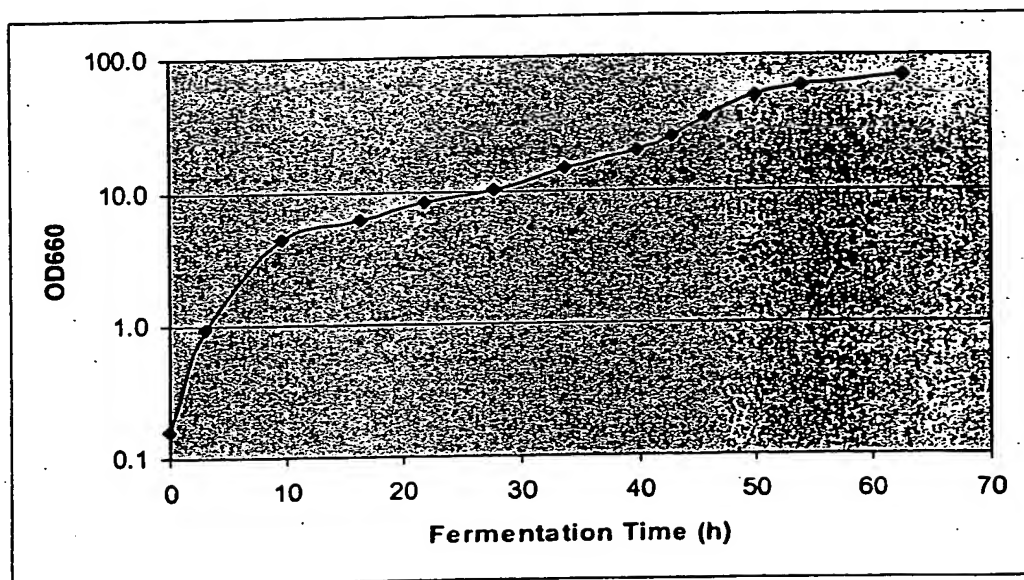


FIG. 11

A.



B.

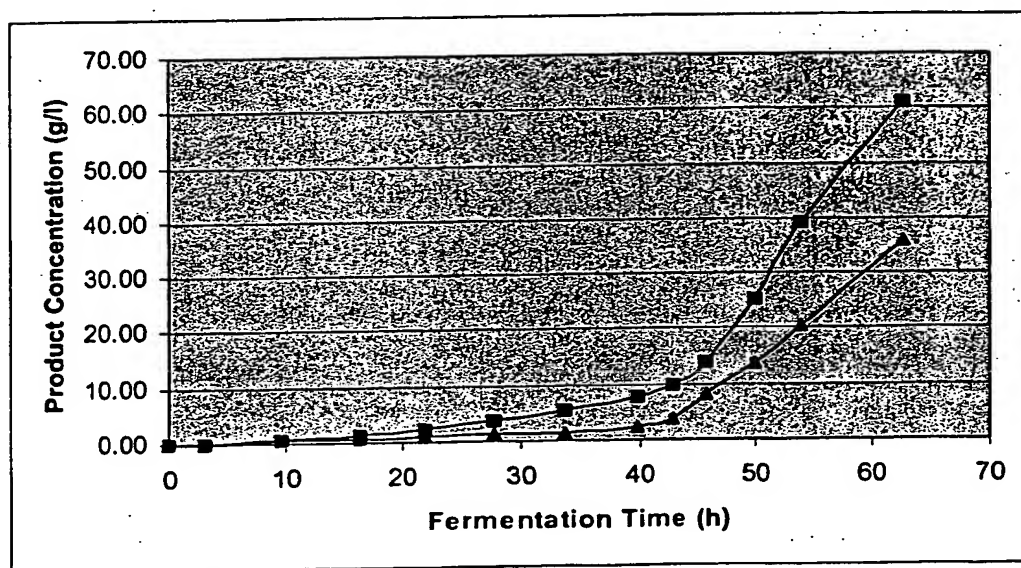
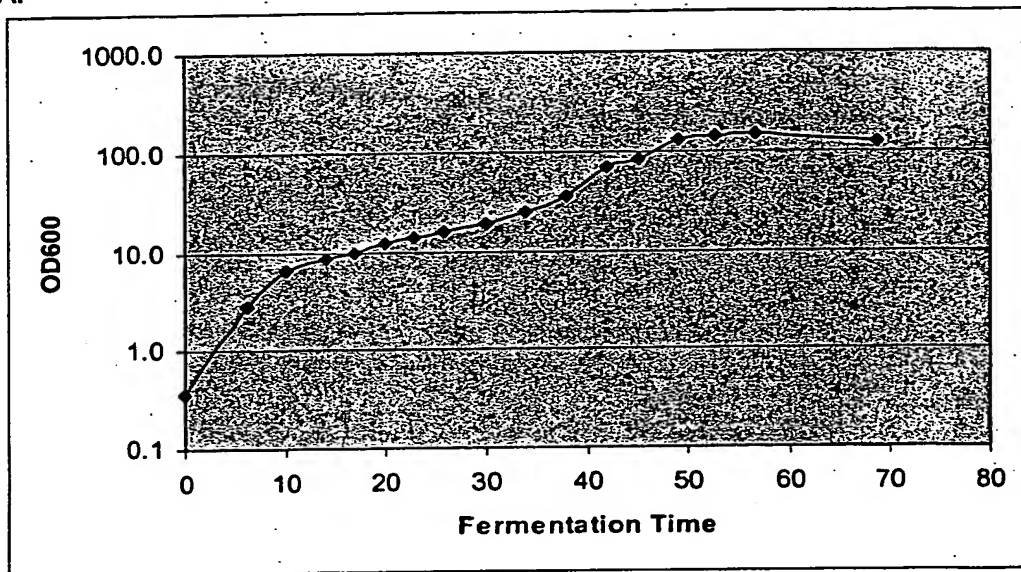
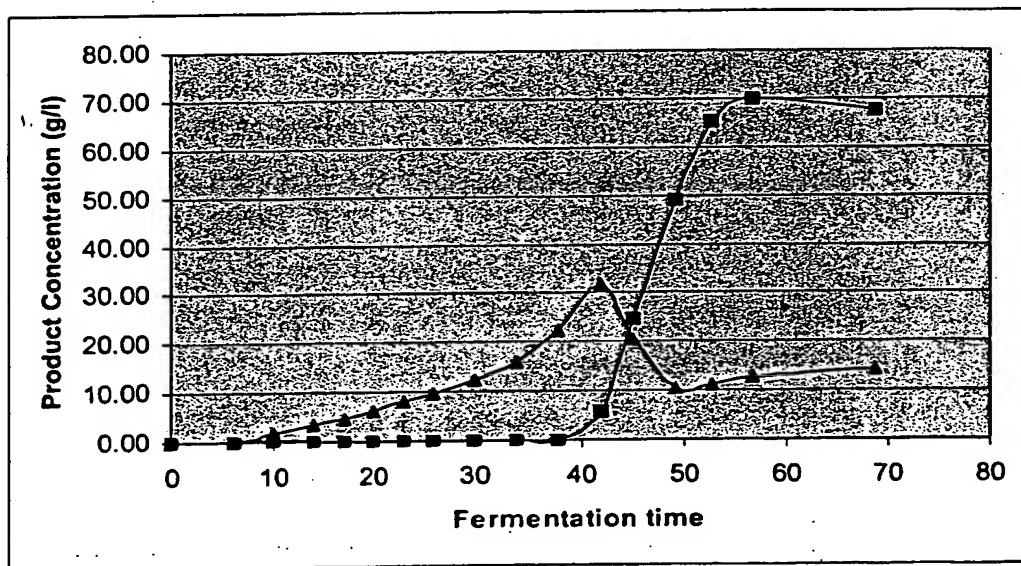


FIG. 12

A.



B.



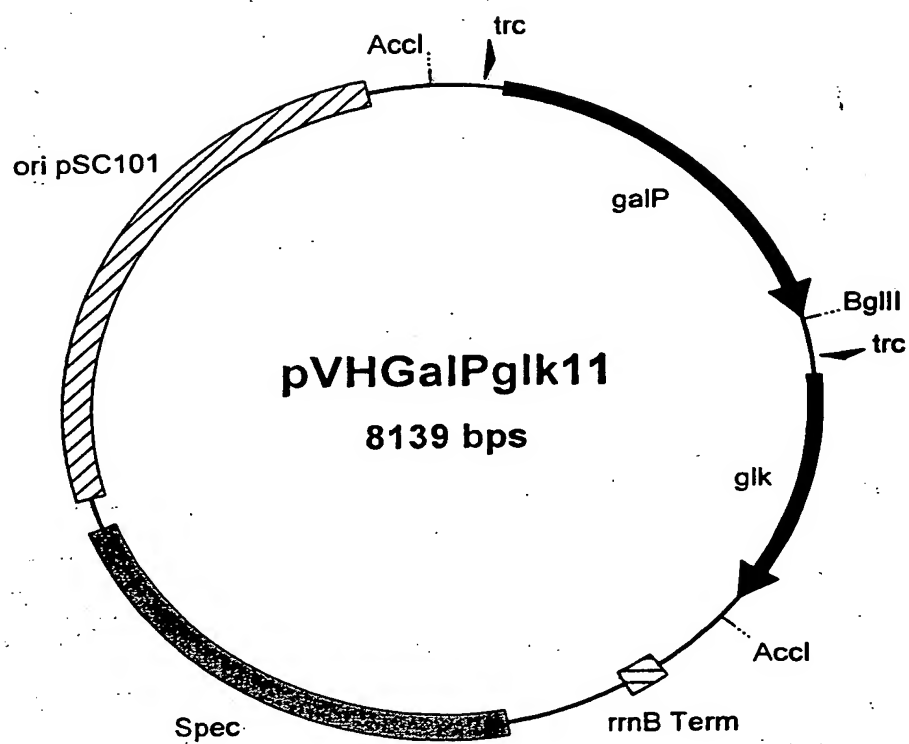


FIG. 13

ATAATTGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTGGCCGACATCAACGGTTCGGCAAATATTCTGAAATGAGCTGTTGACAA 200
TATTAGCACAGCGAGTCCGCGTGAGGGCAAGACCTATTACAAAAACGGCGCTGTAGTATTGCCAAGACCGTTTATAAGACTTTACTCGACAACTGTT

Trc Pro -

TTAATCATCCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACAAATTCACACAGGAACAGACCATGCCTGACGCTAAAAACAGGGCGGTCAAAC 300
AATTAGTAGCGCGAGCATATTACACACCTTAACACCTCGCCTATTGTTAAAGTGTCCTTTGTCTGGTACGGACTCGGATTTTTTGTCCCGCCAGTTTG

Trc Promoter

Met Pro Asp Ala Lys Lys Gln Gly Arg Ser Asn
galP

AAGGCAATGACGTTTTTCGTCTGCTTCCTTCCGCTCTGGCGGATTACTCTTTGGCCTGGATATCGGTGTAATTGCTGGCGCACTGCCGTTTATTGCAG 400
TTCCGTTACTGCAAAAAGCAGACGGAAGAACGGCGAGACCGCCCTAATGAGAAACCGGACCTATAGCCACATTAAACGACCGCTGACGGCAATAACGTC

Lys Ala Met Thr Phe Phe Val Cys Phe Leu Ala Ala Leu Ala Gly Leu Leu Phe Gly Leu Asp Ile Gly Val Ile Ala Gly Ala Leu Pro Phe Ile Ala
galP

ATGAATTCAGATTACTTCGCACACGCAAGAATGGTCTGAAGCTCCATGATGTTGCGTGGCAGTCGGTGGCAGCGGCTGCTCTCTTTAA 500
TACTTAAGGTCTAATGAAGGTGCTGCTTACCAGCATTCGAGGTACTACAAGCCACCGCTCAGCCACCGCTCGCCGACCGAGAGAAAT

Asp Glu Phe Gln Ile Thr Ser His Thr Gln Glu Trp Val Val Ser Ser Met Met Phe Gly Ala Ala Val Gly Ser Gly Trp Leu Ser Phe Lys
galP

ACTCGGGCGCAAAAGAGCCCTGATCGGGCGCAATTTTGTGTCGGGTTGCTCTGCGGCTGCGCCAAACGTTGAAGTACTGATTCCTTTCC 600
TGAGCCCGCGTTTTTCTCGGACTACTAGCCGCGTTAAACAAACAGGCCAAGCAGACAAAGAGACCGCGCGGTTTGCAACTTCATGACTAAGAAAGG

Leu Gly Arg Lys Lys Ser Leu Met Ile Gly Ala Ile Leu Phe Val Ala Gly Ser Leu Phe Ser Ala Ala Pro Asn Val Glu Val Leu Ile Leu Ser
galP

CGCGTTCTACTGGGGTGGCGGTGGCTCTTATACCGCACCGCTGTACCTCTCTGAAATTCGCGCGGAAAAAATTCGTGGCAGTATGATCTCGA 700
GCGCAAGATGACCCCGACCGCCACCCGAGAAATATGGCGTGGCGACATGGAGAGACTTTAACGCGGCCCTTTTTTAAGCACCGTCTACTAGAGCT

Arg Val Leu Leu Gly Leu Ala Val Gly Val Ala Ser Tyr Thr Ala Pro Leu Tyr Leu Ser Glu Ile Ala Pro Glu Lys Ile Arg Gly Ser Met Ile Ser
galP

FIG. 14A

IGIATCAGIIGAIACALAIUUGGAIUCCUGGIGUCTIATICTTTCIGATACCGGCTTCAGGATACCGGCTTACGACCCACACTAATA
ACATAGTCAACTACTAGTAGCCCTAGGAGCCACGAATAGAAAGACTATGGCGGAAGTCGATGTGCCACGTACCGGACCTACCGGACCTACGACCTACGACCTAATA
Met Tyr Gln Leu Met Ile Thr Ile Gly Ile Leu Gly Ala Tyr Leu Ser Asp Thr Ala Phe Ser Tyr Thr Gly Ala Trp Arg Trp Met Leu Gly Val Ile Ile

CATCCCGGCAATTTTGTGCTGATTGGTGCTCTTCTTCCTGCCAGACAGCCACAGTTGGTTTGCCGCCAAACGCCGTTTTTGTGATGCCGAACGCGTGCTG 900
GTAGGGCCGTTAAACGACGACTAACCCACAGAGAAGGACGGTCTGTCTGGGTGCAACCAACGCGGTTTGCGGCCAAACAACTACGGCTTGCGCACGAC
Ile Pro Ala Ile Leu Leu Ile Gly Val Phe Phe Leu Pro Asp Ser Pro Arg Trp Phe Ala Ala Lys Arg Arg Phe Val Asp Ala Glu Arg Val Leu

CTAGCCCTGCGTGACACCAGCGGGAAGCGAAACGGAACCTGGATGAAATCCGTGAAAGTTTGCAGGTTAAACAGAGTGGCTGGCGCTGTGTTAAAGAGA 1000
GATCGGACGCACTGTGGTCGGCCTTCGCTTGGCTTGACCTACTTTAGGCACCTTTCAAACGTCCAAATTTGTCTCACCAGCCCGCACAAATTTCTCT
Leu Arg Leu Arg Asp Thr Ser Ala Glu Ala Lys Arg Glu Leu Asp Glu Ile Arg Glu Ser Leu Gln Val Lys Gln Ser Gly Trp Ala Leu Phe Lys Glu

ACAGCAACTCCGCGCGGGTGTTCTTGGCGTACTGTGTCAGGTAATGCAGCAATTCACGGGATGAACGTCATCATGTATTACGCGCCGAAAAATCTT 1100
TGTCGTTGAAGGCGCGGCCACAAGAACCGCATGACAACGTCCATTACGTCGTTAAGTGGCCCTACTTGCAGTAGTACATAATGCGGCTTTTAGAA
Asn Ser Asn Phe Arg Ala Val Phe Leu Gly Val Leu Leu Gln Val Met Gln Gln Phe Thr Gly Met Asn Val Ile Met Tyr Ala Pro Lys Ile Phe

CGAACTGGCGGGTTATACCAACACTACCGAGCAAAATGTGGGGACCGTGATTGTGGCCTGACCAACGTACTTGCCACCTTTATCGCAAATCGGCTTGTT 1200
GCTTGACCGCCCAATATGTTGTGATGGCTCGTTTACACCCCTGGCACTAACAGCGGACTGTTGCATGAACGGTGGAAATAGCGTTAGCCGGAACAA
Glu Leu Ala Gly Tyr Thr Asn Thr Thr Glu Gln Met Trp Gly Thr Val Ile Val Gly Leu Thr Asn Val Leu Ala Thr Phe Ile Ala Ile Gly Leu Val

GACCGCTGGGACGTAAACCAACGCTAACGCTGGGCTTCCTGGTGATGGCTGGCATGGCGGTACTCGGTACAATGATGCATATCGGTATTCACCTCTC 1300
CTGGCGACCCCTGCATTGTGCGATTGCGACCCGGAAGGACCCTACCGACGACCGTACCCGCGCATGAGCCATGTTACTAGCTATAGCCATAAGTGAGAG
Asp Arg Trp Gly Arg Lys Pro Thr Leu Thr Thr Leu Phe Leu Val Met Ala Ala Gly Met Gly Val Leu Gly Thr Met Met His Ile Gly Ile His Ser

CGTCGGCGCAGTATTCGCCATGCCATGCTGCTGATGTTTATTGTGGTTTGCCATGAGTGCCGGTCCGCTGATTTGGGTACTGTGCTCCGAAATTCA 1400
GCAGCGCGGTCAATAAGCGGTAGCGGTACGACGACTACAAATAACAGCCAAACGGTACTCAGCGCCAGGCGGACTAAACCCATGACACGAGGCTTTAAGT
Pro Ser Ala Gln Tyr Phe Ala Ile Ala Met Leu Leu Met Phe Ile Val Gly Phe Ala Met Ser Ala Gly Pro Leu Ile Trp Val Leu Cys Ser Glu Ile Gln

FIG. 14B

CCGCGACTTTCGGCGCTAAACCGTAGTGGACGAGGTGCTGCTAACGGTTGTACTAGCAACCGGTTGCAAGGACITGGTACGAGTTGTGC
 Pro Leu Lys Gly Arg Asp Phe Gly Ile Thr Cys Ser Thr Ala Thr Asn Trp Ile Ala Asn Met Ile Val Gly Ala Thr Phe Leu Thr Met Leu Asn Thr
 _____galp_____

CTGGGTAACGCCAACACCTTCTGGGTGTATGCGGCTCTGAACGTACTGTTTATCCTGCTGACATTGTGGCTGGTACCGGAAACCAACACAGTTTCGCTGG 1600
 GACCCATTGCGGTTGTGGAAGACCCACATAGCCGAGACTTGCAATGACAAATAGGACGACTGTAAACACCGACCATGGCCTTTGGTTTGTGCAAGCGGACC
 Leu Gly Asn Ala Thr Phe Trp Val Tyr Ala Ala Leu Asn Val Leu Phe Ile Leu Leu Thr Trp Leu Val Pro Glu Thr Lys His Val Ser Leu
 _____galp_____

AACATATTGAACGTAATCIGATGAAAGGTGCTAAACTGCGGAAATAGGCGCTCACGATTAACTCCCCAAGCTTCCCTCCCATGCGGAGGAAACCCACCT 1700
 TTGTATAACTTGCATTAGACTACTTTCAGCAATTTGACGCGCTTATCCGCGAGTGCTAAATTAGAGGGGTTCGAAGGAGGGTAGCGCTCCTTTGGTGGA
 Glu His Ile Glu Arg Asn Leu Met Lys Gly Arg Lys Leu Arg Glu Ile Gly Ala His Asp
 _____galp_____

CTGCGAGTCAICTTTTTCGCTCTATCCTCIGCCGCTAATCCATATGACTAGATCTGCAGAAATTCGCCCTTAAGGAAGCTGTGGTATGGCTGTGCAGGT 1800
 GAACGTCAGTAGAAAAGAAGCGGAGATAGGAGCGGCGATTAGGTATACTGATCTAGACGTCTTAAGCGGGAAATTCCTTCGACACCATACCGACACGTCCTCA
 CGTAAATCAGTCATAATTGCTGTGGCTCAAGGGCGCACICCCGTTCTGGATAATGTTTTTGGCCGACATCATACGGTTCTGGCAAATATTCTGAAAT 1900
 GCATTTAGTGACGTATTAAAGCACAGCGAGTTCGCGGTGAGGGCAAGACCTATTACAAAAACGGGCTGTAGTATGCCCAAGACCGTTTATAAGACTTTA
 GAGCTGTTGACAAATTAATCATCCGGCTCGTATAATGTGTGGAAATTGTGAGCGGATAACAAATTCACACAGGAACAGACCATGACAAAGTATGCATTAGT 2000
 CTCGACAACTGTTAATTAGTAGCCGAGCATATTACACACCTTAACACTCGCCTATTGTTAAAGTGTGCTCTTTGCTGGTACTGTTTCATACGTAATCA
 Met Thr Lys Tyr Ala Leu Val
 _____glk_____

CCGTGATGTGGGCGCACCAACGCACGCTTGTGCTGTGTGATATTGCCAGTGGTGAAATCTCGCAGGCTAAGACCTATTTCAGGGCTTGATTACCCCCAGC 2100
 GCCACTACACCCGCGGTGGTGGTGCAGAACGAGACACACTATAACGGTCACCACCTTAGAGCGTCCGATTCTGGATAAGTCCCGAATAATGGGGTGC
 Gly Asp Val Gly Thr Asn Ala Arg Leu Leu Cys Asp Ile Ala Ser Gly Glu Ile Ser Gln Ala Lys Thr Tyr Ser Gly Leu Asp Tyr Pro Ser
 _____glk_____

CTCGAAGCGGTCATTGCGGTTTATCTTGAAGAACATAAGGTGAGGTGAAAGACGGCTGTATTGCCATCGCTTGCCCAATTACCGGTGACTGGGTGGCGA 2200
 GAGCTTCGCCAGTAAGCGCAATAGAACTTCTTGTTATTCAGCTCCACTTCTGCGGACATAACGGTAGCGAAGGGTTAATGGCCACTGACCCACCCGCT
 Leu Glu Ala Val Ile Arg Val Tyr Leu Glu Glu His Lys Val Glu Val Lys Asp Gly Cys Ile Ala Ile Ala Cys Pro Ile Thr Gly Asp Trp Val Ala
 _____glk_____

FIG. 14C

ACTGGTTGGTATGGACCCGCAAGAGTTAACGGCTTTACTTTTTCTTAGAGCCAAAATCGGTAGACCTTTAATAATTGCTAAAAATGGCGACATAGCTACCG
 yet Thr Asn His Thr Trp Ala Phe Ser Ile Ala Glu Met Lys Lys Asn Leu Gly Phe Ser His Leu Glu Ile Ile Asn Asp Phe Thr Ala Val Ser Met Ala
 _____gln_____

GAACCCGATGCTGAAAAAGAGCATCTGATTCAGTTTGGTGGCGCAGAACCGGTGCAAGGTAAAGCCTATTGCGGTTTACGGTGCCTGGGAACGGGGCTTGGG 2400
 CTTGGGCTACGACTTTTTTCTCGTAGACTAAGTCAAAACCCGCGTCTTGGCCAGCTTCCATTGCGATAACGCCAAAATGCCACGGCCTTGCCCCGAAACCC
 Asn Pro Met Leu Lys Lys Glu His Ile Gln Phe Gly Ala Glu Pro Val Glu Gly Lys Pro Ile Ala Val Tyr Gly Ala Gly Thr Glu Leu Gly
 _____gln_____

GTTGGCATCTGGTCCATGTCGATAAGCGTTGGTAAGCTTGCCAGGCGAAGGCGGTACAGTTGATTTTGGCGCCGAATAGTGAAGAAGAGGCCATTATCC 2500
 CAACCGGTAGACCAGGTACAGCTATTCCGAACCCATTCCGAACGGTCCGCTTCCGCCAGTGCACCTAAACCGCGCTTATCATTCTTCTCCGGTAAATAGG
 Val Ala His Leu Val His Val Asp Lys Arg Trp Val Ser Leu Pro Gly Glu Gly His Val Asp Phe Ala Pro Asn Ser Glu Glu Ala Ile Ile
 _____gln_____

TCGAAATATTGGTGGCGGAAAATTGGTTCATGTTTCGGCGGAGGCGTGCCTTTTCTGGCCCTGGGCTGGTGAATTTGTATCGCGCAATTGTGAAAGCTGACAA 2600
 AGCTTTATAACGCACGCCCTTTAACCCAGTACAAAGCCGCTCCGCACGGAAGACCCGGACCCGACCACCTTAAACATAGCGGTTAACACCTTTCGACTGTT
 Leu Glu Ile Leu Arg Ala Glu Ile Gly His Val Ser Ala Glu Ala Cys Leu Ser Gly Pro Gly Leu Val Asn Leu Tyr Arg Ala Ile Val Lys Ala Asp Asn
 _____gln_____

CCGCTGCCAGAAAAATCTCAAGCCAAAAGATATTACCGAACGGCGCTGGCTGACAGCTGCACCGATTGCCGCCGCGCATTTGTGCTGTTTGGTGCATT 2700
 GCGGACGGTCTTTTAGAGTTTGGTTTCTATAATGGCTTGGCGCGGACCGACTGTCGACGTGGCTAACGGCGCGTAACAGCGACAAAACGCAGTAA
 Arg Leu Pro Glu Asn Leu Lys Pro Lys Asp Ile Thr Glu Arg Ala Leu Ala Asp Ser Cys Thr Asp Cys Arg Ala Leu Ser Leu Phe Cys Val Ile
 _____gln_____

ATGGGCGGTTTTGGCGCAATCTGGCGCTCAATCTCGGACATTTGGCGCGGTGTTTATTGGCGCGGTATCGTGCCTGCTTCCCTTGTAGTTCTTCAAAG 2800
 TACCCGGCAAAACCGCGTTAGACCGCGAGTTAGAGCCCTGTAAACCGCGCACAAAATAACGCCGCCCATAGCACGGCGCGGAAGAACTCAAGAAGTTTC
 Met Gly Arg Phe Gly Asn Leu Ala Leu Asn Leu Gly Thr Phe Gly Gly Val Phe Ile Ala Gly Ile Val Pro Arg Phe Leu Glu Phe Phe Lys
 _____gln_____

GCTCCGGTTTTCCGTGCCGCAATTGAAGATAAAGGGCGCTTAAAGAAATATGTCCATGATATTCCGGTGTATCTCATCTGTCCTGACAAATCCGGGCTTCT 2900
 CGAGGCCAAAGGCACGGCGTAACTTCTATTTCGCCGGAATTTCTTATACAGGTACTATAAGGCCACATAGAGTAGCAGGTACTGTAGGCCCGGAAGA
 Gly Ser Gly Phe Arg Ala Ala Phe Glu Asp Lys Gly Arg Phe Lys Glu Tyr Val His Asp Ile Pro Val Tyr Leu Ile Val His Asp Asn Pro Gly Leu Leu
 _____gln_____

CCGCTCCGCTGACATTTAGGCTCAGGCTGGAATCCAGTGTAGACATTTAGGAGGAAATATAGCCCTCCATTGAGAGGGCTATTAGAAAAATTTAGTATGT
GCCAAGGCCACGCTGTAATGCGGCTCTGGATCCAGTGTAGACATTTAGGAGGAAATATAGCCCTCCATTGAGAGGGCTATTAGAAAAATTTAGTATGT

Gly Ser Gly Ala His Leu Arg Gln Thr Leu Gly His Ile Leu •

glk

GTTTATTCAATTTTTCTTTGTGTCCCTCACAAGGTCGAC 3040
CAATAAGTTAAAAAGAAACACAGGGGAGTGTCCAGCTG